

**Fig. 1A**

G	S	V	A	C	P	P	P	A	Y	C	N	T	P	P	P	P	Y	E	166								
GGG	AGT	GTG	GCC	TGC	CCG	CCC	CCT	CCA	GCC	TAC	TGC	AAC	ACG	CCT	CCG	CCC	TAC	GAA	632								
Q	V	V	K	A	K	*														173							
CAG	GTA	GTG	AAG	GCC	AAG	TAG														653							
TGG	GTG	CCCA	CGT	GCA	GAG	GAG	GAG	AGG	CCCTT	CCCT	GGCC	TTT	CTG	TCT	TCG	TTG	ATG	TTCA	CCAG	732							
GAAC	GGT	CTC	GTG	GGC	TGCT	AAG	GCAG	TTT	CCCT	CTG	ATA	TCC	TCAC	AGCA	AGCA	CAG	CTCT	CTT	CAGG	CTTCC	ATGG	811					
AGT	ACA	ATAT	ATGA	ACT	CAC	ACT	TTG	TCT	CTCT	GTG	TTT	CTG	TTT	CTG	ACG	CAG	CTCT	GTG	CTCT	CAC	ATGG	890					
GGT	GAC	AGT	CCCC	GAG	GGCT	GAC	GTCC	TTAC	GGT	GGCT	GAC	CCAG	ATCT	AC	AGAG	AGAG	ACTG	AGAG	GAAG	AAAG	GCAG	969					
TGCT	GGAG	GTG	CAG	GTG	GCAT	GTAG	AGGG	CCAG	CCG	CAG	CAT	CCC	AGG	CAAT	CC	TCTG	CCCC	GGT	ATTA	ATAG	1048						
AAG	CCC	ATG	CCG	GGC	GCT	CAG	CCG	ATGA	AGC	AGC	AGC	CCG	ACTG	AG	CTG	AGCC	CAG	CAG	GTCA	TCTG	CTCC	AGC	CTGT	1127			
CCT	CTC	GTAG	CCCT	TCT	CCAG	AA	AGCT	TTT	CGA	AG	CA	TTT	CGA	AG	CA	TTT	CGA	AG	CA	TTT	CGA	AG	CA	TTT	1206		
CTGT	TCAT	ATC	CTAA	AGAT	AGACT	TTCT	CC	TGC	AC	CCG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	AGG	1285		
CTAG	AA	TCAG	GCCT	TG	AG	GCCT	GAC	AGT	ATCT	GAC	ATCC	AT	CCAC	TA	AG	CA	AA	TTT	AT	TA	AT	TCAT	GG	AA	ATCA	1364	
CTT	CC	TG	CCCC	AA	CTG	AG	CA	TTT	GT	AG	CTCT	TT	GG	CT	GT	AT	TT	GG	AA	AG	AG	ACTG	TAC	CC	ATTT	TTTG	1443
GTGT	TTAT	GGAA	GTG	ATG	ATG	AGCG	TC	CTG	CCCT	TT	GAA	ATC	AG	ACT	GGG	GTG	GTG	CTT	CCC	TG	GAC	ATCA	CTGC	1522			
CTCT	CCAG	GGCAT	TTCT	CAG	GGC	GGGG	TC	CTC	CTC	AGG	CA	CTC	AG	CTC	AG	CTC	AG	CTC	AG	CTC	AG	CTC	AG	CTC	AG	CTC	1601
ACGG	GGCAC	ATCT	GGC	TGG	AA	GT	CAC	ATG	GA	CTCT	CC	AGG	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	1680	
GT	TGGG	CTAA	CGGG	GTG	TG	CTG	GGCT	CC	AG	GAG	GAG	CTT	CTG	GG	AA	AG	AG	AG	AG	AG	AG	AG	AG	AG	AG	1759	
TGCA	CTG	ACCAT	GTG	TCATA	AT	TAGA	ATA	AA	AG	AA	AG	AGT	GGT	CG	AA	ATG	CAC	AT	CC	TG	GAT	AG	AA	TCAC	AGCTCA	1838	
CCCC	AGG	ATCT	CAC	AGG	ATG	CTC	CTG	AGT	AGT	TG	AG	CTG	AG	GGG	AG	CTAG	T	CC	CC	CC	AG	ATAG	TATAG	GTG	TGA	1917	
TGT	GTGA	ACG	CTG	AC	CTG	TCT	CTG	CTA	AG	AG	CTA	TG	CAG	CT	TAG	CTG	AG	GG	CC	CTAG	AT	TACT	AG	ATG	CTGTAT	1996	
CAC	GGGA	ATG	AGG	TGGG	GTG	CTT	ATTT	TTA	ATG	AA	CTA	AT	CAG	AG	CCCT	CTT	GAG	AA	AT	TG	TACT	CA	TTG	AACTGG	2075		
AGCA	TCAG	ACAT	CTCA	TGGA	GTG	GAT	ACG	GAG	TGAT	TTG	GTG	TCC	ATG	CTTT	TCA	CTCT	GAG	GAC	ATTT	AA	TCGG	AG	ATTT	AA	TCGG	AG	2154

Fig. 1B

AACCTCCTGGGAAATTTGTGGGAGACACTTGGGAACAAAACAGACACCCCTGGGAATGCAGTTGCAAGCACAGATGCTG 2233  
 CCACCAGTGTCTCTGACCACCCCTGGTGTGACTGCTGACTGCCAGCGGTACCTCCCATGCTGCAGGCCCTCCATCTAAA 2312  
 TGAGACAAACAAAGCACAAATGTTCACTGTTTACAACCAAGACAACTGCGTGGTCCAAACACTCCTCTTCTCCAGGTCA 2391  
 TTTGTTTGTGCAATTTTAAATGTCCTTTATTTTGTAAATGAAAAAGCACACTAAGCTGCCCCCTGGAATCGGGTGCAGCTGA 2470  
 ATAGGCACCCAAAAGTCCGTGACTAAAATTTTCGTTTGTCTTTTGTATAGCAAAATATGTTAAAGAGACAGTGGCTAGG 2549  
 GCTCAACAAATTTTGTAATTTCCCATGTTTGTGTGAGACAGAGTTTGTTCCTTGAACCTTGGTTAGAAATGTGCTACTGT 2628  
 GAACGCTGATCCTGCATATGGAAGTCCCACTTTGGTGACATTTCTTGGCCATTCTTGTTCATTTGTGTGGATGGTGGG 2707  
 TTGTGCCCCACTTCCCTGGAGTGAGACAGCTCCTGGTGTAGAAATCCCGGAGCGTCCGTGGTTCAGAGTAAACTTGAAG 2786  
 CAGATCTGTGCATGCTTTTCTCTCTGCAACAAATTTGGCTCGTTTCTCTTTTGTCTCTTTTGTATAGGATCCTGTTTCTT 2865  
 ATGTGTGCAAAATAAAAAATAAATTTGGCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 2944  
 AAAAAAAGGGGGCGCGC 2964

Fig. 1C

GTCGACCCACGCGTCCGGCCGCGGTCTTCTGCGGGCTTCAGCTCGTATCCCCGGAGTCCACCCGCCGTCCCGGGGT 79  
 GCGGACTGGCCCTGAGCTGGCCGTACAGCCCCGGCTTCGGACGGTCCCTCGCTGGAGCC ATG GGC CGC CGG CTC 151  
 M G R R L 5  
 G R V A A L L L G L L V E C T E A K K H 25  
 GGC AGG GTG GCG CTG CTG CTC GGG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT 211

Fig. 1D

C W Y F E G L Y P T Y Y I C R S Y E D C 45  
TGC TGG TAT TTT GAA GGA CTC TAT CCC ACA TAC TAT ATA TGC CGT TCC TAT GAA GAC TGC 271

C G S R C C V R A L S I Q R L W Y F W F 65  
TGT GGC TCC AGG TGC TGT GTG AGG GCC CTT TCC ATA CAG AGG CTG TGG TAT TTT TGG TTC 331

L L M M G V L F C C G A G F I R R M 85  
CTG CTG ATG ATG GGT GTG CTG TTC TGC TGT GGT GCC GGT TTC ATT CGC CGG CGC ATG 391

Y P P P L I E E P T F N V S Y T R Q P P 105  
TAT CCG CCA CCA CTC ATT GAG GAG CCC ACA TTC AAT GTG TCC TAT ACC AGG CAG CCA CCA 451

N P A P G A Q Q M G P P Y Y T D P G P 125  
AAT CCT GCT CCA GGA GCA CAG CAA ATG GGA CCG CCA TAT TAC ACC GAC CCT GGA GGA CCC 511

G M N P V G N T M A M A F Q V Q P N S P 145  
GGG ATG AAT CCT GTT GGC AAT ACC ATG GCT ATG GCT TTC CAG GTC CAG CCC AAT TCA CCT 571

H G G T T Y P P P P S Y C N T P P P Y 165  
CAC GGA GGC ACA ACT TAC CCA CCC CCT CCT TCC TAC TGC AAC ACG CCT CCA CCC CCC TAT 631

E Q V V K D K \* 173  
GAA CAG GTG GTG AAG GAC AAG TAG 655

CAAGATGCTACATCAAAGGCAAGAGGATGGACAGGCCCTTTTGTATTACCTTCCCATCCTCACCAGATACTTGCTGATAG 734

**Fig. 1E**

GGTGGTCCAAGGGAAACTTGGATATTCTCAAGCAAGCCAGCTCTCTTCAAGTCTTTTGTGGAGACATTTGAATC 813  
CACACTGTCTCCTCTGTGCTTCTGATGTAGTCTGTGCTCTCTGAGAGAGTGTGGCAACAGTCCCTGAGGGTT 892  
GATATTCTAGGGTGTCCAGGGTAGATCCTCGGAGAGAGGCTAAGGGAAAGGAAGGATAGCCTGTGTAGGGG 971  
CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACCTTCGAAGAGACACTATCCACCA 1050  
TCCCAGCCCATTTCTCCTAATAGAAAGCTGTGGGCTGTGTTGTTGATGCTCTTTTGGTCTCCACTCACATTTTGAATAAG 1129  
GCTTTCTCTGCAGGAATAGGAAAGACCCAAAGTACATATTGTGCTTCCACTTAAATAAGGGTCAAGAACAGGCCTCAG 1208  
TTGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTAAAGTTAGGGGAAATTTCTCTAAATGGAGACATT 1287  
GCGTTTTATGAATCATCGTCTGGCTTTTCTTTAGTGCATGATTGAAGTGAGGGTGTCTCTTTGAGATCAGATGGGGAG 1366  
AGTGAACCTCTGCGGGGGTGGGTGTCTCTACTCAGAGGGCTCCAAACCCCTTTTCTTAGGTAGTTCTGGTATGGGT 1445  
TTATGGGCACTATAGAGCTGAGGGGCACATTAGCCGGGTAGTTACATTTGACCTTTGGAGAGGAAGAGACAGCCAAAG 1524  
AAACTCAGCAAAGCAAGACCAGCATTTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTCTGGCCTCA 1603  
GAAGAGGGACGTTTGTGGATAGAGCCGTGAAAACCTACTTAGTTGCACAGATGACATAATCAAAAAGTAGAGAAAAG 1682  
TGTAAGTTAGAGATGCCATTTCCAGGTGAGAAATCAGAGCTCATCCATAGATTTACAAAGTAGTGGCTGGAGTTAACAGTA 1761  
TGGAGTTCTTTTCCCTTGCCTAGTTAGTCACGTTGATGTGATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA 1840  
GGAAGTATAGCTAAGATGTCTAGATTATTTATATGATGATGTTGGGAGTGGGCTGCAAGGAAGGGGCTGACATTG 1919  
TAAATGAGAAAAATCAGAGCCATTTGATAAACTGTTACTTGTGGATCAGGCATCCAAAAGTGTCTCTTGTAGTGGACATT 1998  
GAGTATTCTTTACCACTACAAGACCAGGAGGATGGTGTCTCTCCATTGGGGTATTTATATGAGGTAGAGGTTTCAG 2077  
GAATCGACAGTAGTGTGGGCTTAGTTTAAGGACTGAAAGCATAGGACTGTAGACAGTTTCATAGGAAACTGCGG 2156  
GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCCATCATTTGAGCACCCCTTGTGTCTCTGGC 2235  
TTCTGTCTACTGGATCCAGTACCCCTCCATGCTTGGTCCCTTGTTTACATAAGACAAACAAAGCACAAATGTCTGTGTT 2314  
TACAATCAAGACGACTACATGGTCCAAACATTTCTCTCTTCTATCATTGTGGCTTTAACTTCCATTTCCTCCGTT 2393  
CCTTTTAAATCAAGAAAGCACAGTCAGAGCTGCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTTCAGTGTG 2472  
CATGACTAAATCTTATCTTTTGTATAGCAAAATCCTTTTAAAGAAACTGAACAAATGCTAAGGCTCAGCAATTTTATACTC 2551  
CAATGTCTGTGAAGGTAAATTTTGTGTCATTTGAGCCCAATTTGGAATTCCTTCTGACGTCAACACTGACAAATGCCT 2630  
ATGGAAATTGCACCTTCTGGGTATATGTCCAGCATCCTTGTCTTATGTTTGTGTAGTAAGGCTCACCCCTTCCAGC 2709

**Fig. 1F**

AGCTCTACTTCTGTGCTGAGGTCCTGTAGAGCCGGGCTTGGGCACAGACATGAGGCAGACTTGTGCATGCTCTTC 2788  
 TTGGCAACACTTGCTCATAATTCTTCTCTTTGATAGATCCTGTTTCCCTATGTATTTAAAAATAATAAAGTG 2867  
 AATTAGTCAAAAAAAAAAAAAAAAAAGGGCGCGCGC 2915

**Fig. 1G**

	10	20	30	40	50	60	70
Hum.	MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYICRSYEDCCGSRCCVRALS	QRLWYFWFLMMG					
	:	:	:	:	:	:	:
Mur.	MGRRLGRVAALLLGLLVECTEAKKHCWYFEGLYPTYICRSYEDCCGSRCCVRALS	QRLWYFWFLMMG					
	10	20	30	40	50	60	70
	80	90	100	110	120	130	140
Hum.	VLFCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGGAQQPGPPYTD	PGGMNPGNSMAMAFQV					
	:	:	:	:	:	:	:
Mur.	VLFCGAGFFIRRRMYPPPLIEEPTFNVSYTRQPPNAPGAQQMGPPYTD	PGGMNPGNTMAMAFQV					
	80	90	100	110	120	130	140
	150	160	170				
Hum.	PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK						
	:	:	:	:	:	:	:
Mur.	QPNSPHGGTTYPPPPSYCNTPPPPYEQVVKDK						
	150	160	170				

**Fig. 1H**

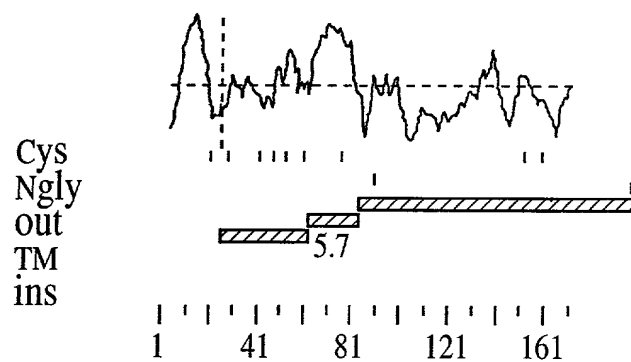


Fig. 1I

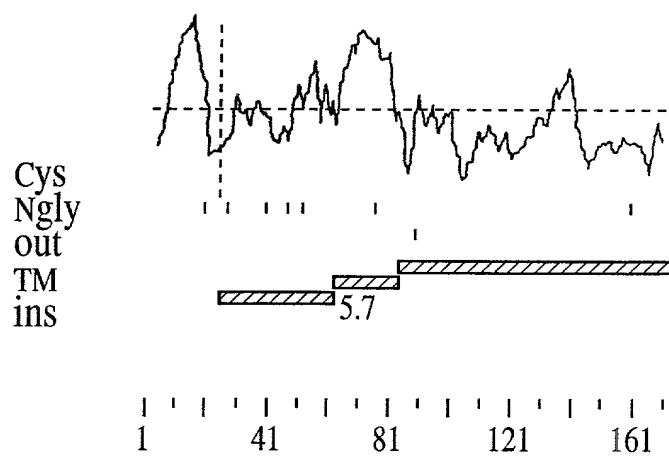


Fig. 1J

GTCGACCCACGCGTCCGGAAATGTCGTTCTTCAGATTAAAAAGAAACCTTTACTGAATCAGCTGAGTGTTAATAATA	79
CGAATTTCCTTTCTTGCCAATTCTGATCTGAACAGAAAAATCCAAGAACAGGGAT	152
M C G L Q F	6
ATG TGT GGA TTA CAG TTT	
S L P C L R L F L V V T C Y L L L L L H	26
TCT CTG CCT TGC CTA CGA CTG TTT CTG GTT ACC TGT TAT CTT TTA TTA CTC CAC	212
K E I L G C S S V C Q L C T G R Q I N C	46
AAA GAA ATA CTT GGA TGT TCG TCT GTT TGT CAG CTC TGC ACT GGG AGA CAA ATT AAC TGC	272
R N L G L S S I P K N F P E S T V F L Y	66
CGT AAC TTA GGC CTT TCG AGT ATT CCT AAG AAT TTT CCT GAA AGT ACA GTT TTT CTG TAT	332
L T G N N I S Y I N E S E L T G L H S L	86
CTG ACT GGG AAT AAT ATA TCT TAT ATA AAT GAA AGT GAA TTA ACA GGA CTT CAT TCT CTT	392
V A L Y L D N S N I L Y V Y P K A F V Q	106
GTA GCA TTG TAT TTG GAT AAT TCT AAC ATT CTG TAT GTA TAT CCA AAA GCC TTT GTT CAA	452
L R H L Y F L F L N N N F I K R L D P G	126
TTG AGG CAT CTA TAT TTT CTA AAT AAT AAT TTC ATC AAA CGC TTA GAT CCT GGA	512

Fig. 2A



"CGFQ" TESTED

I	F	K	G	L	L	N	L	R	N	L	Y	L	Q	Y	N	Q	V	S	F	146
ATA	TTT	AAG	GGA	CTT	TTA	AAT	CTT	CGT	AAT	TTA	TAT	TTA	CAG	TAT	AAT	CAG	GTA	TCT	TTT	572
V	P	R	G	V	F	N	D	L	V	S	V	Q	Y	L	N	L	Q	R	N	166
GTT	CCG	AGA	GGA	GTA	TTT	AAT	GAT	CTA	GTT	TCA	GTT	CAG	TAC	TTA	AAT	CTA	CAA	AGG	AAT	632
R	L	T	V	L	G	S	G	T	F	V	G	M	V	A	L	R	I	L	D	186
CGC	CTC	ACT	GTC	CTT	GGG	AGT	GGT	ACC	TTT	GTT	GGT	ATG	GTT	GCT	CTT	CGG	ATA	CTT	GAT	692
L	S	N	N	N	I	L	R	I	S	E	S	G	F	Q	H	L	E	N	L	206
TTA	TCA	AAC	AAT	AAC	ATT	TTG	AGG	ATA	TCA	GAA	TCA	GGC	TTT	CAA	CAT	CTT	GAA	AAC	CTT	752
A	C	L	Y	L	G	S	N	N	L	T	K	V	P	S	N	A	F	E	V	226
GCT	TGT	TTG	TAT	TTA	GGA	AGT	AAT	AAT	TTA	ACA	AAA	GTA	CCA	TCA	AAT	GCC	TTT	GAA	GTA	812
L	K	S	L	R	R	L	S	L	S	H	N	P	I	E	A	I	Q	P	F	246
CTT	AAA	AGT	CTT	AGA	AGA	CTT	TCT	TTG	TCT	CAT	AAT	CCT	ATT	GAA	GCA	ATA	CAG	CCC	TTT	872
A	F	K	G	L	A	N	L	E	Y	L	L	L	K	N	S	R	I	R	N	266
GCA	TTT	AAA	GGA	CTT	GCC	AAT	CTG	GAA	TAC	CTC	CTC	CTG	AAA	AAT	TCA	AGA	ATT	AGG	AAT	932
V	T	R	D	G	F	S	G	I	N	N	L	K	H	L	I	L	S	H	N	286
GTT	ACT	AGG	GAT	GGG	TTT	AGT	GGA	ATT	AAT	AAT	CTT	AAA	CAT	TTG	ATC	TTA	AGT	CAT	AAT	992

**Fig. 2B**

D L E N L N S D T F S L L K N L I Y L K 306  
 GAT TTA GAG AAT TTA AAT TCT GAC ACA TTC AGT TTG TTA AAG AAT TTA ATT TAC CTT AAG 1052  
  
 L D R N R I I S I D N D T F E N M G A S 326  
 TTA GAT AGA AAC AGA ATA ATT AGC ATT GAT AAT GAT ACA TTT GAA AAT ATG GGA GCA TCT 1112  
  
 L K I L N L S F N N L T A L H P R V L K 346  
 TTG AAG ATC CTT AAT CTG TCA TTT AAT AAT CTT ACA GCC TTG CAT CCA AGG GTC CTT AAG 1172  
  
 P L S S L I H L Q A N S N P W E C N C K 366  
 CCG TTG TCT TCA TTG ATT CAT CTT CAG GCA AAT TCT AAT CCT TGG GAA TGT AAC TGC AAA 1232  
  
 L L G L R D W L A S S A I T L N I Y C Q 386  
 CTT TTG GGC CTT CGA GAC TGG CTA GCA TCT TCA GCC ATT ACT CTA AAC ATC TAT TGT CAG 1292  
  
 N P P S M R G R A L R Y I N I T N C V T 406  
 AAT CCC CCA TCC ATG CGT GGC AGA GCA TTA CGT TAT ATT AAC ATT ACA AAT TGT GTT ACA 1352  
  
 S S I N V S R A W A V V K S P H I H H K 426  
 TCT TCA ATA AAT GTA TCC AGA GCT TGG GCT GGT GTA AAA TCT CCT CAT ATT CAT CAC AAG 1412  
  
 T T A L M M A W H K V T T N G S P L E N 446  
 ACT ACT GCG CTA ATG ATG GGC TGG CAT AAA GTA ACC ACA AAT GGC AGT CCT CTG GAA AAT 1472

Fig. 2C

Figure 2D

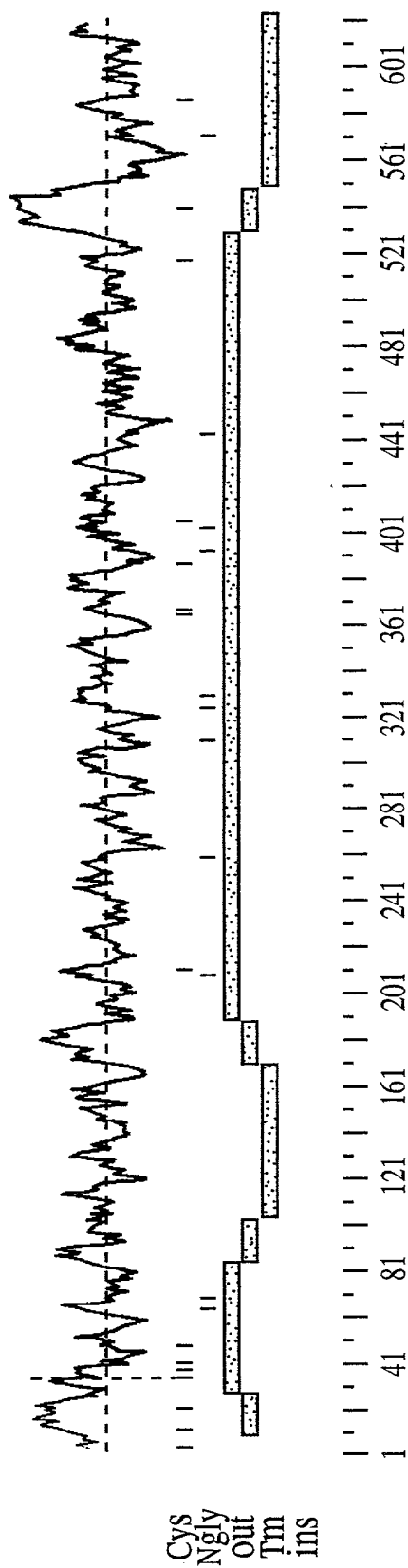
T	E	T	E	N	I	T	F	W	E	R	I	P	T	S	P	A	G	R	F	466
ACT	GAG	ACT	GAG	AAC	ATT	ACT	TTC	TGG	GAA	CGA	ATT	CCT	ACT	TCA	CCT	GCT	GGT	AGA	TTT	1532
F	Q	E	N	A	F	G	N	P	L	E	T	T	A	V	L	P	V	Q	I	486
TTT	CAA	GAG	AAT	GCC	TTT	GGT	AAT	CCA	TTA	GAG	ACT	ACA	GCA	GTG	TTA	CCT	GTG	CAA	ATA	1592
Q	L	T	T	S	V	T	L	N	L	E	K	N	S	A	L	P	N	D	A	506
CAA	CTT	ACT	ACT	TCT	GTT	ACC	TTG	AAC	TTG	GAA	AAA	AAC	AGT	GCT	CTA	CCG	AAT	GAT	GCT	1652
A	S	M	S	G	K	T	S	L	I	C	T	Q	E	V	E	K	L	N	E	526
GCT	TCA	ATG	TCA	GGG	AAA	ACA	TCT	CTA	ATT	TGT	ACA	CAA	GAA	GTT	GAG	AAG	TTG	AAT	GAG	1712
A	F	D	I	L	L	A	F	F	I	L	A	C	V	L	I	I	F	L	I	546
GCT	TTT	GAC	ATT	TTG	CTA	GCT	TTT	TTC	ATC	TTA	GCT	TGT	GTT	TTA	ATC	ATT	TTT	TTG	ATC	1772
Y	K	V	V	Q	F	K	Q	K	L	K	A	S	E	N	S	R	E	N	R	566
TAC	AAA	GTT	GTT	CAG	TTT	AAA	CAA	AAA	CTA	AAG	GCA	TCA	GAA	AAC	TCA	AGG	GAA	AAT	AGA	1832
L	E	Y	Y	S	F	Y	Q	S	A	R	Y	N	V	T	A	S	I	C	N	586
CTT	GAA	TAC	TAC	AGC	TTT	TAT	CAG	TCA	GCA	AGG	TAT	AAT	GTA	ACT	GCC	TCA	ATT	TGT	AAC	1892
T	S	P	N	S	L	E	S	P	G	L	E	Q	I	R	L	H	K	Q	I	606
ACT	TCC	CCA	AAT	TCT	CTA	GAA	AGT	CCT	GGC	TTG	GAG	CAG	ATT	CGA	CTT	CAT	AAA	CAA	ATT	1952

Fig. 2D

V P E N E A Q V I L F E H S A L \* 623  
GTT CCT GAA AAT GAG GCA CAG GTC ATT CTT TTT GAA CAT TCT GCT TTA TAA 2003  
CTCAACTAAATATTGTCATATAAGAAACTTCAGTGCCATGGACATGATTAAACTGAAACCTCCTTATATAATTATATAC 2082  
TTTAGTTGAAAATATAATGAATTATATGAGGTTAGCATTATTAAATATGTTTTTAATAAAAAAAAAAAAAAAGG 2161  
GCGGCCGC 2169

**Fig. 2E**

FOSTO 1499.60



Cys  
Ngly  
out  
tm  
ins

FIG. 2F

```

10  MRGVGWQMLSLSLGLVLA-----ILNKVAPQACPAQCS-CSGSTVDCHGLALRSVPRNIPRNTERLDLNG
: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 MCGLQFSLPCLRLFLVVTCYLLLLHKK-EILGCSSVCQLCTGRQINCRNLGLSSIPKNFPESTVFLYLTG
10  20 30 40 50 60

70  NNITRITKDFAGLRHLRVLQLMENKISTIERGAFQDLKELERLRLNRNHLQLFPPELLFLGTAKLYRLDL
: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 NNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLR-----HLY--FLFLNNNFIKRLD-
70  80 90 100 110 120 130

140 SENQIQAIPRKAFRGAVDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASFNHMPKLRTF
: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 -----PGI-----FKGLLNLRNLYLQYNQVSFVPRGVFNDLVSVQYLNLRNRLTVLGSQTF-----
130 140 150 160 170 180 190 200

210 RLHSNNLYCDCHLAWLSDWLRQRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSGHQSFMAPSCSVLHCP
: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 -----VGM-----VA-----
180

```

Fig. 2G

# Fig. 2H

```

280      290      300      310      320      330      340
Slit AACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQNTIKVIPPGAFSPYKKLRRIDLSNNQISELAPDAF
325 -----
      :: :: :: :: ::
      LRILDSNNNI-----
      190

350      360      370      380      390      400      410
Slit QGLRSLNSLVLYGNKITELPKSLFEGFLSLQLLLNANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAG
      :: :: :: :: ::
325 --LR-----ISE-----SGFQHLENLACL-----
      200

420      430      440      450      460      470      480
Slit TFSPLRAIQTMHLAQNPFCDCHLKWLADYLHTNPIETSGARCTSPRRLANKRIGQIKSKKFRCSAKEQY
      :: ::
325 -----YLGSN-----
      210

490      500      510      520      530      540      550
Slit FIPGTEDYRSKLSGDCFADLACPEKCRCEGTTVDCSNQKLNKIPEHIPOYTAELRLNNNEFTVLEATGIF
325 -----
      :: :: :: :: ::
      NLTKVP-----SNAFEVLKS-----
      220

```

**Fig. 2H**





```

      840      850      860      870      880      890      900
Slit  GNDISVVPEGAFNDLSALSHLAIGANPLYCDNCNMQLSDWVKSEYKEPGIARCAGPGEMADKLLITTPSK
      325  -----SSLIHLQANSNPWECNCKLLGLRDWLAS-----
           350      360      370

      910      920      930      940      950      960      970
Slit  KFTCQGPVDVNILAKCNPCLSNPCKNDGTCNSDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCH
           ... ..:
      325  -----SAITLNI-----Y-----CQNP-----PSMRG-----
           380                                390

      980      990     1000     1010     1020     1030     1040
Slit  LKEGEEDGFWCICADGFEGENCEVNVDDCEDNDCENNSTCVVDGINNYTCLCPPEYTGELCEEKLDFCAQD
           ... :
      325  -----RALRYI-----NITNCV-----
           400

     1050     1060     1070     1080     1090     1100     1110
Slit  LNPCQHDSKCILTPKGFKCDCTPGYVGEHCDIDFDDCQDNKCKNGAHCTDAVNGYTCICPEGYSLFCEF
           .....:
      325  -----TSSIN-----
           410

```

Fig. 2J



# Figure 2L

```

1400      1410      1420      1430      1440      1450      1460
Slit  SCKCLEGHGGVLCDEEEDLFNPCQAICKKHGKCRLSGLGQPYCECSSGYTGDSCDREISCRGERIRDYYQ
      .:      .:      .:      .:      .:      .:      .:
325 AC-----VL-----IIFLIYKVVQFKQ---KLKA-----SENS-----RENRL-EYY-
      540      550      560      570

1470      1480      1490      1500      1510      1520
Slit  KQQGYAACQTTK-KVSRLECRGGCAGGCCGGLRSKRRKYSFECTDGSSFVDEVEKVVKCGCTRCVS
      ..      :.... :.. :      .:      .:      .:      .:
325 ---SF---YQSARYNVVTASICNTSPNSLESPPGLEQIRLHK-----QIVPENEAQVI-LFEHSAL
      580      590      600      610      620

```

**Fig. 2L**

```

10      20      30      40      50      60      70
Slit  CAGAGCAGGTTGAGAGGCGGTGGAGCGGTGTCCTGAGTGGGCTCTACTGCCTTGTTCCATATT
325  -----

      80      90      100     110     120     130     140
Slit  TTGTGCACATTTCCCTGGCACTCTGGGTGCTAGCCCCGCCGGCACTGGGCCCTCAGACACTGCGCGGT
325  -----

150     160     170     180     190     200     210
Slit  TCCCTCGGAGCAGCAAGCTAAAGAAAGCCCCCAGTGCCCGCGGAGGAAGAGCGCGGGGAAAGATGCGC
325  -----

220     230     240     250     260     270     280
Slit  GCGTTGGCTGCAGATGCTGCCCTGTCGCTGGGTTAGTGCTGGCGATCCTGAACAAGGTGCACCGC
      ::::
325  -----GTCG-----ACC--

```

**Fig. 2M-1**

Figure 2M-2

```

290      300      310      320      330      340      350
Slit AGCGTGCCCGCGCAGTGCTCTTGCTCGGCAGCACAGTGGACTGTACGGGCTGGCGCTGCGCAGCGT
325 -----CACG-----CGT
                               10

360      370      380      390      400      410      420
Slit GCCCAGGAATATCCCCGCAACACCGAGAGACTGGATTAAATGGAATAACATCACAAGAATTACGAAG
      :::::::::::
325 --CCGGAATGTC-----
                               20

430      440      450      460      470      480      490
Slit ACAGATTTTGCTGGTCTTAGACATCTAAGAGTTCTTCAGCTTATGGAGAAATAAGATTAGCACCATTTGAAA
      :::::::::::
325 -----GTTCTTCAGATTTAAAAAGAAAA-----CCTTTA---
                               30      40      50

500      510      520      530      540      550      560
Slit GAGGAGCATTCAGGATCTTAAAGAACTAGAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTCC
      :::::::::::
325 -----CTGAATC-----AGCT-GAGTG-----TTAAT---AATACG-----AATTTC
                               60      70      80
```

Fig. 2M-2

**Fig. 2M-3**

# Figure 2M-4

```

850      860      870      880      890      900      910
Slit  TGTACTGCCACCTGGCCTGGCTCTCCGACTGGCTTCGCCAAGCCTCGGGTTGGTCTGTACTCAGT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
325  TATTACT-CCACAAAG-----AAATAC-----TTGGA-TGTTTCG-TC--T
      210      220      230

920      930      940      950      960      970      980
Slit  GTATGGGCCCCCTCCACCTGAGAGGCCATAATGTAGCCGAGGTTCAAAAACGAGAAATTTGTCTGCAGTGG
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
325  GTTTG-----TC-----AGC-----TCTGCACTGG
      240      250

990      1000     1010     1020     1030     1040     1050
Slit  TCACCAGTCATTATGGCTCCTTCTTGTAGTGTTTTGCACTGCCCTGCCGCTGTACCTGTAGCAACAAT
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
325  G-----AGACAAATTA-----ACTGCC-----GTAACCTTAGGC-----
      260      270      280

1060     1070     1080     1090     1100     1110     1120
Slit  ATCGTAGACTGTCGTGGGAAAGGTCTCACTGAGATCCCCACAAATCTTCCAGAGACCATCACAGAAATAC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
325  -----CTTTCGAG-----TATTC---CTAAGA-----ATTTTCCCTGAAA--GT-ACAGTTTTC
      290      300      310      320

```

**Fig. 2M-4**

**Fig. 2M-5**



```

1480      1490      1500      1510      1520      1530      1540
Slit  CAAACTATGCATTGGCCCAAGACCCCTTATTGTGACTGCCATCTCAAGTGGTAGCGGATTATCTCC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
325  CAAAC---GC-TTAGATCCTGGA-----ATATT-----AAGGACTTT---TAAATCTTC
      500      510      520      530

```

	1620	1630	1640	1650	1660	1670	1680
Slit	ACAGATCAAAAGCAAGAAATTCGGTTGTT	CAGCTAAAGAACAGTATTTCA	TTCCAGTACAGAAAGATTAT				
	::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::						
325	ACAGT--ATAATCAGGTA--TC	TTTTGTTTC--CGAGAGG--AGTATTTAAT	-----				
	560	570	580	590			

**Fig. 2M-6**

**Fig. 2M-7**

```

170 180 190 200 210 220 230
Slit AAATACTTCTTACGAGTAATCGTTTGAAAATGTCAGCATAAGATGTTCAAGGGATTGGAAAGCCTCAA
      :: :: :: :: :: ::
325 --ATACTT-----GATTATC-----A
      690

240 250 260 270 280 290 300
Slit AACTTTGATGTTGAGAAGCAATCGAATAACCTGTGTGGGAATGACAGTTTCATAGGACTCAGTTCTGTG
      :: :: :: :: :: ::
325 AAC-----AATAAC--ATTTGAGGATATCAGAAATCAG-----
      700      710      720

2110 2120 2130 2140 2150 2160 2170
Slit CGTTTGCTTCTTGTATGATAATCAAAATTACTACAGTTCACCCAGGGCATTTGATACTCTCCATCTT
      :: :: ::
325 -----GCTTTC-----
      730

2180 2190 2200 2210 2220 2230 2240
Slit TATCTACTCTAAACCTCTTGGCCCAATCCTTTTAACTGTAACCTGCTACCTGGCTTGGTGGGAGAGTGGCT
      :: :: :: :: :: ::
325 -----AACATCTTGA--AAACCTT-----GCTTGTGTTGTAT-----T
      740      750      760

```

Fig. 2M-8



# Figure 2M-10

```

2530      2540      2550      2560      2570      2580      2590
slit CTCCTCAACTACAAACATTTAAACACTTATAGACTTAAAGTAACAACAGATAAGCACGCTTCTTAATCAGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 ---TCCTGAAAAAATTCAAGAA-----TTAGGA---ATGTTACTA-GGGATGGG-----TTTAGT--GG
      910      920      930      940      950

2600      2610      2620      2630      2640      2650      2660
slit GCTTCAGCAACATGACCCAGCTCCTCACCTTAATCTTAGTTACAACCGCTGAGATGTATTCCTCCTCG
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 AATTAAATAATCTTAA-----ACATTGATCTTAA-----GTCA-TAATGA-----
      960      970      980      990

2670      2680      2690      2700      2710      2720      2730
slit CACCTTTGATGGATTAAAGTCTCTTCGATTACTTCTCTACATGGAAATGACATTTCTGTGTGCCTGAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 ----TTTAGAGAAATTTAAAT-----TCTGACACATTCAGT--TTGTTAAAGA-ATT--TAATTACCTTAA
      1000     1010     1020     1030     1040     1050

2740      2750      2760      2770      2780      2790      2800
slit GGTGCTTTCAATGATCTTTCTGCAATTATCACATCTAGCAATTGGAGCCAACCCCTCTTTACTGTGATTGTA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 G-----TTAGATAGAA---ACAGAAATAAT-----TAGCATT-----GATAATGAT
      1060     1070     1080

```

**Fig. 2M-10**

```

2810      2820      2830      2840      2850      2860      2870
slit ACATGCAGTGGTTATCCGACTGGGTGAAGTCGGAATATAAGGAGCCTGGAATTGCTCGTTGTGCTGGTCC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 ACAT-----TTGAAAATATGGGAGCAT-----CTTTGAA--GATCC
1090      1100      1110

2880      2890      2900      2910      2920      2930      2940
slit TGGAGAAATGGCAGATAAACTTTTACTCACAACCTCCCTCCAAAAAATTACCTGTCAAGGTCCTGTGGAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 T-----TAATCTGTCA-----
1130

2950      2960      2970      2980      2990      3000      3010
slit GTCAATATCTAGCTAAGTGTAAACCCCTGCCCTATCAAATCCGTGTAAAAATGATGGCACATGTAATAGTG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 -TTAATAATCTTACA-----GCCTTGC--ATCCAAG-----G
1140      1150      1160

3020      3030      3040      3050      3060      3070      3080
slit ATCCAGTTGACTTTTACCGGATGCACCTGTCCATATGGTTTCAAGGGGCAGGACTGTGATGTCCCAATTCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325 GTCC-----TTAAGCCGT-----TGTC-----TTCATTG-----ATTCA
1170      1180      1190

```

Fig. 2M-11

Figure 2M-12

```

3090      3100      3110      3120      3130      3140      3150
Slit  TGCCTGCATCAGTAACCCATGTAACATGGAGAACTTGCCACTTAAAGGAGGAGAAAGATGGATTC
:      ::::      ::::      ::::      ::::      ::::      ::::
325 T-----CTTCAG-----CAAATT-----CTAATC-CTT-----GGGAATGTAACCTGCAAAC
1200
3160      3170      3180      3190      3200      3210      3220
Slit  TGGTGTATTGTGCTGATGGATTGGAAGGAGAAAAATTGTGAAGTCAACGTTGATGATGTGAAGATAATG
:      ::::      ::::      ::::      ::::      ::::      :
325 T-----TTTGGGC-----CTTCGA-----G
1240

3230      3240      3250      3260      3270      3280      3290
Slit  ACTGTGAAAAATAATTCTACATGTGTCGATGGCATTAAATAACTACACATGCCCTTGCCACCTGAGTATAC
:      ::::      ::::      ::::      ::::      ::::      :
325 ACTG-----GC-----TAGCAT-----CTTCA---GCCATTAC-----
1250      1260      1270

3300      3310      3320      3330      3340      3350      3360
Slit  AGGTGAGTTGTGTAGGAGAAAGCTGGACTTCTGTGCCCAGGACCTGAACCCCTGCCAGCACGATTCAAAG
:      ::::      ::::      ::::      ::::      ::::      :
325 -----TCTAAACATCTATT-----GTCAGAAATCCCC-----
1280      1290

```

Fig. 2M-12

**Fig. 2M-13**



**Fig. 2M-14**

**Fig. 2M-15**

# Figure 2M-16

```

4210      4220      4230      4240      4250      4260      4270
Slit  TGTGAGCCATGCCACAAGAGTGTGTGCCCATGGCACATGCCAGCCAGCAGCCAGGCGTTACCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325  TTTGATC--TAC-----AAAGTTGTT-----CAGTTTA---A
      1770      1780      1790

4280      4290      4300      4310      4320      4330      4340
Slit  GCGAGTGCCAGGAAGGATGGATGGGGCCCCCTCTGTGACCAACGGACCAATGACCCTTGCCTTGGAAATAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325  ACAAAAATA--AAG-----CATCAGAAAAC-----CAAGGGAAAAAT
      1800      1810      1820

4350      4360      4370      4380      4390      4400      4410
Slit  ATGCGTACATGCGACCTGCTTGCCCATCAATGCGTTCTCCTACAGCTGTAAGTGCTTGGAGGGCCATGGA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325  AGACTTGAATA-CTACAGCTT-----TTATCAGTCAGCAAGGTATA-----ATGTA
      1830      1840      1850      1860      1870

4420      4430      4440      4450      4460      4470      4480
Slit  GGTGTCCTCTGTGATGAAGAGGAGGAGTCTGTTTAACCCATGCCAGGCGATCAAGTGCAAGCACGGGAAGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
325  ACTG-CCTCAAT-TTG-----TAACACTTCCC-----CAAAATTCT--CT-AGAAAGT
      1880      1890      1900      1910

```

**Fig. 2M-16**

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

```

4490      4500      4510      4520      4530      4540      4550
Slit GCAGGCTTTCAGGCTCTGGGCGAGCCCTACTGTGAATGCAGCAGTGGATACACGGGGACAGCTGTGATCG
      :::::      :::::      :::::      :::::      :::::      :::::
325 CCTGGCTT-----GGAGCAG-----ATTC-----GACTTCA-TAAACA
      1920      1930

4560      4570      4580      4590      4600      4610      4620
Slit AGAAATCTCTTGTCTGAGGGGAAAGGATAAGAGATTATTACCAAAAGCAGGCTATGCTGCTTGCCAA
      :::::      :      :::::      :::::      :::::      :::::
325 AATTGT-TC-----TGAAAATGAG-----GCA-CAGGTC-ATTCTTTTGTG---A
      1950      1960      1970      1980

4630      4640      4650      4660      4670      4680      4690
Slit ACAACCAAGAGGTGTCCCGATTAGAGTGCAGAGGTGGGTGTGCAGGAGGGCAGTGCTGTGGACCGCTGA
      :::::
325 ACATTC-----TGCTTTATAACTC---
      1990      2000

4700      4710      4720      4730      4740      4750      4760
Slit GGAGCAAGCGCGGAAATACTCTTTCGAATGCACCTGACGGCTCCTCCTTTGTGGACGAGGTTGAGAAAGT
      :::::      :::::      :::::      :::::      :::::      :::::
325 --AACTAA-----ATATTGTCTATAAGAACT---TCAGTGCCA-----TGGACATGATTTAAA-----
      2010      2020      2030      2040      2050

```

Fig. 2M-17

2060

2080

2140 2150 2160

**Fig. 2M-18**

GCAGCTCTGGGGAGCTCGGAGCTCCCGATCACGGCTTCTTGGGGTAGCTACGGCTGGGTGTGTAGAACGGGGCCGGG 79  
GCTGGGGCTGGGTCCCTAGTGGAGACCCAAAGTGGAGAGGCAAGAACTCTGCAGCTTCTGCTTCTGGGTCAAGTTCC 158  
TTATTCAAGTCTGCAGCCGGCTCCAGGGAGATCTCGGTGGAACCTTCAGAAACGCTGGGCAGTCTGCCTTTCAACC 234

M P L S L G A E M W G P E A W L L L L L L L 20  
ATG CCC CTG TCC CTG GGA GCC GAG ATG TGG GGG CCT GAG GCC TGG CTG CTG CTG CTG CTA 294

L L A S F T G R C P A G E L E T S D V V 40  
CTG CTG GCA TCA TTT ACA GGC CGG TGC CCC GCG GGT GAG CTG GAG ACC TCA GAC GTG GTA 354

T V V L G Q D A K L P C F Y R G D S G E 60  
ACT GTG GTG CTG GGC CAG GAC GCA AAA CTG CCC TGC TTC TAC CGA GGG GAC TCC GGC GAG 414

Q V G Q V A W A R V D A G E G A Q E L A 80  
CAA GTG GGG CAA GTG GCA TGG GCT CGG GTG GAC GCG GGC GAA GGC GCC CAG GAA CTA GCG 474

L L H S K Y G L H V S P A Y E G R V E Q 100  
CTA CTG CAC TCC AAA TAC GGG CTT CAT GTG AGC CCG GCT TAC GAG GGC CGC GTG GAG CAG 534

P P P P R N P L D G S V L L R N A V Q A 120  
CCG CCG CCC CCA AAC CCC CTG GAC GGC TCA GTG CTC CTG CGC AAC GCA GTG CAG GCG 594

**Fig. 3A**

D E G E Y E C R V S T F P A G S F Q A R 140  
 GAT GAG GGC GAG TAC GAG TGC CGG GTC AGC ACC TTC CCC GCC GGC AGC TTC CAG GCG CGG 654

L R L R V L V P P L P S L N P G P A L E 160  
 CTG CGG CTC CGA GTG CTG GTG CCT CCC CTG CCC TCA CTG AAT CCT GGT CCA GCA CTA GAA 714

E G Q G L T L A S C T A E G S P A P S 180  
 GAG GGC CAG GGC CTG ACC CTG GCA GCC TCC TGC ACA GCT GAG GGC AGC CCA GCC CCC AGC 774

V T W D T E V K G T T S S R S F K H S R 200  
 GTG ACC TGG GAC ACG GAG GTC AAA GGC ACA ACG TCC AGC CGT TCC TTC AAG CAC TCC CGC 834

S A A V T S E F H L V P S R S M N G Q P 220  
 TCT GCT GCC GTC ACC TCA GAG TTC CAC TTG GTG CCT AGC CGC AGC ATG AAT GGG CAG CCA 894

L T C V V S H P G L L Q D Q R I T H I L 240  
 CTG ACT TGT GTG GTG TCC CAT CCT GGC CTG CTG CAG GAC CAA AGG ATC ACC CAC ATC CTC 954

H V S F L A E A S V R G L E D Q N L W H 260  
 CAC GTG TCC TTC CTT GCT GAG GAG TCT GTG AGG GGC CTT GAA GAC CAA AAT CTG TGG CAC 1014

I G R E G A M L K C L S E G Q P P S Y 280  
 ATT GGC AGA GAA GGA GCT ATG CTC AAG TGC CTG AGT GAA GGC CAG CCC CCT CCC TCA TAC 1074

**Fig. 3B**

N	W	T	R	L	D	G	P	L	P	S	G	V	R	V	D	G	D	T	L	300
AAC	TGG	ACA	CGG	CTG	GAT	GGG	CCT	CTG	CCC	AGT	GGG	GTA	CGA	GTG	GAT	GGG	GAC	ACT	TTG	1134
G	F	P	P	L	T	T	E	H	S	G	I	Y	V	C	H	V	S	N	E	320
GGC	TTT	CCC	CCA	CTG	ACC	ACT	GAG	CAC	AGC	GGC	ATC	TAC	GTC	TGC	CAT	GTC	AGC	AAT	GAG	1194
F	S	S	R	D	S	Q	V	T	V	D	V	L	D	P	Q	E	D	S	G	340
TTC	TCC	TCA	AGG	GAT	TCT	CAG	GTC	ACT	GTG	GAT	GTT	CTT	GAC	CCC	CAG	GAA	GAC	TCT	GGG	1254
K	Q	V	D	L	V	S	A	S	V	V	V	V	G	V	I	A	A	L	L	360
AAG	CAG	GTG	GAC	CTA	GTG	TCA	GCC	TCG	GTG	GTG	GTG	GTG	GGT	GTG	ATC	GCC	GCA	CTC	TTG	1314
F	C	L	L	V	V	V	V	V	L	M	S	R	Y	H	R	R	K	A	Q	380
TTC	TGC	CTT	CTG	GTG	GTG	GTG	GTG	CTC	ATG	TCC	CGA	TAC	CAT	CGG	CGC	AAG	GCC	CAG	1374	
Q	M	T	Q	K	Y	E	E	E	L	T	L	T	R	E	N	S	I	R	R	400
CAG	ATG	ACC	CAG	AAA	TAT	GAG	GAG	GAG	CTG	ACC	CTG	ACC	AGG	GAG	AAC	TCC	ATC	CGG	AGG	1434
L	H	S	H	H	T	D	P	R	S	Q	P	E	E	S	V	G	L	R	A	420
CTG	CAT	TCC	CAT	CAC	ACG	GAC	CCC	AGG	AGC	CAG	CCG	GAG	GAG	AGT	GTA	GGG	CTG	AGA	GCC	1494
E	G	H	P	D	S	L	K	D	N	S	S	C	S	V	M	S	E	E	P	440
GAG	GGC	CAC	CCT	GAT	AGT	CTC	AAG	GAC	AAC	AGT	AGC	TGC	TCT	GTG	ATG	AGT	GAA	GAG	CCC	1554

Fig. 3C



**Fig. 3D**

TCAAGCAATCCTCGCCTCAGCCTCCCTAGTAGCTGGGACTTTAAGTGTAACACCACTGTGCCCTGCTTTGAATCCTTTA 2715  
 CGAAGAGAAAAAAATTAAGAAAAAGCCTTTAGATTTATCCAAATGTTTACTACTGGGATTGCTTAAAGTGAGGCCCTT 2794  
 CCAACACAGGGGTTAATTCTCTGTGATTGTGAAAAGGGCTACTTCCAAGGCATCTTCATGCAGGCAGCCCTTGGGAG 2873  
 GGCACTGAGAGCTGGTAGAGTCTGAAATTAGGGATGTAGCCTCGTGGTTACTGAGTAAGGTAAAAATTGCATCCACCA 2952  
 TTGTTTGTGATACCTTAGGGAATTGCTTGGAACCTGGTGACAAAGGCTCCTGTTCAAATAGTGGTGTGGGGAGAGAGAGA 3031  
 GCAGTGATTATAGACCGAGAGTAGGAGTTGAGGTGAGGTGAAGGAGGTGCTGGGGTGAGAAATGTCGCCCTTTCCTCC 3110  
 TGGGTTTGGATCACTAATTCAAAGGCTCTTCTGGATGTTTCTCTGGGTTGGGCTGGAGTCAATGAGGTTTATTTTA 3189  
 GCTGGCCCAACCAGATACACTCAGCCAGAAATACCTAGATTTAGTACCCAAACCTCTTCTTAGTCTGAAAATCTGCTGGATT 3268  
 TCTGGCCCTAAGGGAGAGGCTCCCATCCTTCGTTCCCGAGCCAGCTAGGACTTCGAAATGTGGAGCCTGAAGATCTAAGA 3347  
 TCCTAAACATGTACATTTTATGTAAATATGTGCATATTGTGACATAAAATGATATTCTGTTTTTAAATAAACAGACAAAA 3426  
 CTTGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 3505  
 AAAAA 3510

Fig. 3E

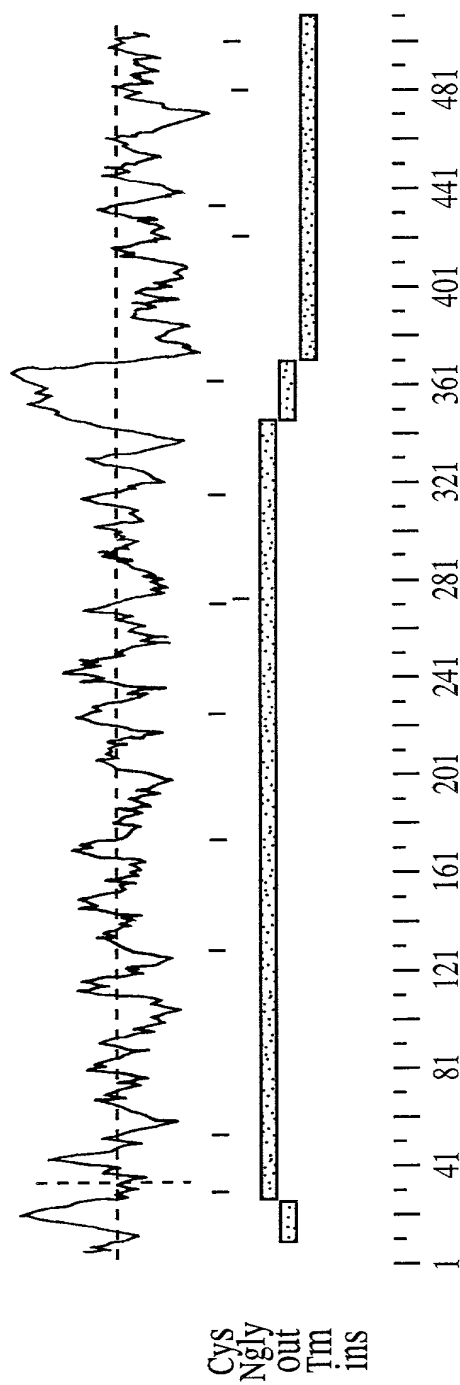


FIG. 3F

K	G	T	T	S	S	R	S	F	K	H	S	R	S	A	A	V	T	S	19	
C	AAA	GGC	ACA	ACG	TCC	AGC	CGT	TCC	TTC	AAG	CAC	TCC	CGC	TCT	GCT	GCC	GTC	ACC	TCA	58
E	F	H	L	V	P	S	R	S	M	N	G	Q	P	L	T	C	V	S	39	
GAG	TTC	CAC	TTG	GTG	CCT	AGC	CGC	AGC	ATG	AAT	GGG	CAG	CCA	CTG	ACT	TGT	GTG	GTG	TCC	118
H	P	G	L	L	Q	D	Q	R	I	T	H	I	L	H	V	S	F	L	A	59
CAT	CCT	GGC	CTG	CTC	CAG	GAC	CAA	AGG	ATC	ACC	CAC	ATC	CTC	CAC	GTG	TCC	TTC	CTT	GCT	178
E	A	S	V	R	G	L	E	D	Q	N	L	W	H	I	G	R	E	G	A	79
GAG	GCC	TCT	GTG	AGG	GGC	CTT	GAA	GAC	CAA	AAT	CTG	TGG	CAC	ATT	GGC	AGA	GAA	GGA	GCT	238
M	L	K	C	L	S	E	G	Q	P	P	P	S	Y	N	W	T	R	L	D	99
ATG	CTC	AAG	TGC	CTG	AGT	GAA	GGG	CAG	CCC	CCT	CCC	TCA	TAC	AAC	TGG	ACA	CGG	CTG	GAT	298
G	P	L	P	S	G	V	R	V	D	G	D	T	L	G	F	P	P	L	T	119
GGG	CCT	CTG	CCC	AGT	GGG	GTA	CGA	GTG	GAT	GGG	GAC	ACT	TTG	GGC	TTT	CCC	CCA	CTG	ACC	358
T	E	H	S	G	I	Y	V	C	H	V	S	N	E	F	S	S	R	D	S	139
ACT	GAG	CAC	AGC	GGC	ATC	TAC	GTC	TGC	CAT	GTC	AGC	AAT	GAG	TTC	TCC	TCA	AGG	GAT	TCT	418
Q	V	T	V	D	V	L	A	D	P	Q	E	D	S	G	K	Q	V	D	L	159
CAG	GTC	ACT	GTG	GAT	GTT	CTT	GCA	GAC	CCC	CAG	GAA	GAC	TCT	GGG	AAG	CAG	GTG	GAC	CTA	478

Fig. 3G

V	S	A	S	V	V	V	V	G	V	I	A	A	L	L	F	C	L	L	V	179
GTG	TCA	GCC	TCG	GTG	GTG	GTG	GTG	GGT	GTG	ATC	GCC	GCA	CTC	TTG	TTC	TGC	CTT	CTG	GTG	538
V	V	V	V	L	M	S	R	Y	H	R	R	K	A	Q	Q	M	T	Q	K	199
GTG	GTG	GTG	GTG	CTC	ATG	TCC	CGA	TAC	CAT	CGG	CGC	AAG	GCC	CAG	CAG	ATG	ACC	CAG	AAA	598
Y	E	E	E	L	T	L	T	R	E	N	S	I	R	R	L	H	S	H	H	219
TAT	GAG	GAG	GAG	CTG	ACC	CTG	ACC	AGG	GAG	AAC	TCC	ATC	CGG	AGG	CTG	CAT	TCC	CAT	CAC	658
T	D	P	R	S	Q	S	E	E	P	E	G	R	S	Y	S	T	L	T	T	239
ACG	GAC	CCC	AGG	AGC	CAG	AGT	GAA	GAG	CCC	GAG	GGC	CGC	AGT	TAC	TCC	ACG	CTG	ACC	ACG	718
V	R	E	I	E	T	Q	T	E	L	L	S	P	G	S	G	R	A	E	E	259
GTG	AGG	GAG	ATA	GAA	ACA	CAG	ACT	GAA	CTG	CTG	TCT	CCA	GGC	TCT	GGG	CGG	GCC	GAG	GAG	778
E	E	D	Q	D	E	G	I	K	Q	A	M	N	H	F	V	Q	E	N	G	279
GAG	GAA	GAT	CAG	GAT	GAA	GGC	ATC	AAA	CAG	GCC	ATG	AAC	CAT	TTT	GTT	CAG	GAG	AAT	GGG	838
T	L	R	A	K	P	T	G	N	G	I	Y	I	N	G	R	G	H	L	V	299
ACC	CTA	CGG	GCC	AAG	CCC	ACG	GGC	AAT	GGC	ATC	TAC	ATC	AAT	GGG	CGG	GGA	CAC	CTG	GTC	898
*																				
TGA																				
																				300
																				901

Fig. 3H

CCCAGGCCCTCCCTTCCCTAGGCCCTGGCTCCTTCTGTGACATGGGAGATTTTAGCTCACTTTGGGGCCCTCCTTA 980  
 AACACCCCAATTTCTTGGGAAGATGCTCCCATCCACTGACTGCTTGACCTTTACCTCCAACCCCTTCTGTTCATCGG 1059  
 GAGGGCTCCACCAATTGAGTCTCTCCACCATGCAATGCAAGTCACTGTGTGTCATGTGTCCTGTGTGAGTGTGA 1138  
 CTGACTGTGTGTGGAGGGGTGACTGTCCGTGGAGGGGTGACTGTGTCCGTGGTGTATATGCTGTCAATATCAG 1217  
 AGTCAAGTGAACGTGGTGTATGTGCCACGGGATTTGAGTGGTTCGCTGGGCAACACTGTGTCAGGGTTTGGCGTGTGT 1296  
 CATGTGGCTGTGTGACCTCTGACCTGAAAAGACAGGATTTTCTCAGACCCAGAGCAGTATTAATGATGCAGAGGTT 1375  
 GGAGGAGAGGTGGAGACTGTGGCTCAGACCCAGGTGTGCGGCATAGCTGGAGCTGGAATCTGCCCTCCGGTGTGAGG 1454  
 GAACCTGTCTCCTACCACTTCGGAGGCCATGGGGCAAGTGTGAAGCAGCCAGTCCCTGGGTCAAGCCAGAGGCTTGAACT 1533  
 GTTACAGAAAGCCCTCTGCCCTCTGGTGGCTCTGGGCCCTGCTGCATGTACATATTTCTGTAAATATACATGCGCCGGG 1612  
 AGCTTCTTGCAAGGAATACTGCTCCGAATCACATTTAAATTTTCTTTTCTTGCCCTTTCCATTAGTTGTATT 1691  
 TTTTATTATTATTTTATTATTTTATTAGAGATGGAGTCTCACTATGTTGCTCAGGCTGGCCTTGAACCTCCTGGGC 1770  
 TCAAGCAATCCTCCTGCTCAGCCTCCCTAGTAGCTGGACTTTAAGTGTACACCACTGTGCCCTGCTTTGAATCCTTTA 1849  
 CGAAGAGAAAAAAAATTAAGAAAGCCCTTAGAATTTATCCAATGTTTACTACTGGGATTGCTTAAAGTGAGGCCCT 1928  
 CCAACACAGGGGTTAATTCCCTGTGATTGTGAAAGGGCTACTTCCAAGGCATCTTCATGCAGGCAGCCCTTGGGAG 2007  
 GGCACCTGAGAGCTGGTAGAGTCTGAAATTAGGGATGTGAGCCTGGTGACAAGGCTCCTGTTCAATAGTGGTGTGGG 2086  
 GAGAGAGAGCAGTGATTATAGACCGAGAGAGTAGGAGTTGAGGTGAGGTGAAGGAGGTGCTGGGGTGAGAAATGTCG 2165  
 CCTTCCCCCTGGGTTTGGATCACTAATTCAAGGCTCTTCTGGATGTTTCTCTGGGTGGGGCTGGAGTCAATGAGG 2244  
 TTATTTTTTAGCTGGCCCCACCCAGATACACTCAGCCAGAAATACCTAGATTAGTACCCAAACTCTTCTTAGTCTGAAAT 2323  
 CTGCTGGATTCTGGCCCTAAGGGAGAGGCTCCCATCCTTCGTTCCCGAGCCAGCTAGGACTTCGAATGTGGAGCCCTGA 2402  
 AGATCTAAGATCCTAACATGTACATTTTATGTAAATATGTGCATATTTGTACATAAAATGATATTCTGTTTTAAATAA 2481  
 ACAGACAAAACCTTGAAAAAATAAAAAA 2510

Fig. 3I

**Fig. 3J**

Figure 3K

```

100      110      120      130      140      150      160
ALT  NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFFSSRDSQVTVDVLADPQEDSGKQVDLVSAS
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
T364 NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFFSSRDSQVTVDVL-DPQEDSGKQVDLVSAS
      290      300      310      320      330      340

170      180      190      200      210      220
ALT  VVVVGVIALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQ-----
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
T364 VVVVGVIALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQPEESVGLR
      350      360      370      380      390      400      410

420      230      240      250      260      270
ALT  -----SEEPEGRSYSTLTTVREIETQTTELLSPGSGRAEEEEEDQDEGIKQAMNHFVQEN
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
T364 AEGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTTELLSPGSGRAEEEEEDQDEGIKQAMNHFVQEN
      430      440      450      460      470      480

280      290
ALT  GTLRAKPTGNGIYINGRGHLV
      ::::::::::::::::::::::::::::::::::::::
T364 GTLRAKPTGNGIYINGRGHLV
      490      500      510

```

Fig. 3K



CTTAAATGTTGGAAGTCTCTTAGTCCCTATGAGAGTGTGTAGCAGTTTGTCCCTGAG	55
CTCTAGCTTCTTTTAAATGAAAGCTGAGTCTCTGGCAACATCTTTAGGGAGAGAGGTACAAAAGTTTCTCTGGACCTTCTC	134
M M Q E Q Q Q P Q S T E K R G W	15
AACACAGGAGCCTGCATA ATG ATG CAA GAG CAG CAA CCT CAA AGT ACA GAG AAA AGA GGC TGG	198
L S L R L W S V A G I S I A L L S A C F	35
TTG TCC CTG AGA CTC TGG TCT TGG GTG GCT GGT GGG ATT TCC ATT GCA CTC CTC AGT GCT TGC TTC	258
I V S C V T Y H F T Y G E T G K R L S	55
ATT GTG AGC TGT GTA GTA ACT TAC CAT TTT ACA TAT GGT GAA ACT GGC AAA AGG CTG TCT	318
E L H S Y H S S L T C F S E G T K V P A	75
GAA CTA CAC TCA TAT CAT TCA AGT CTC ACC TGC TGC TTC AGT GAA GGG ACA AAG GTG CCA GCC	378
W G C C P A S W K S F G S S C Y F I S S	95
TGG GGA TGT TGC CCA GCT TCT TCT TGG AAG TCA TTT GGT TCC AGT TGC TAC TTC ATT TCC AGT	438
E E K V W S K S E Q Q N C V E M G A H L V	115
GAA GAG AAG GTT TGG TCT AAG AGT GAG CAG AAC TGT GTT GAG ATG GGA GCA CAT TTG GTT	498
V F N T E A E Q Q N F I V Q Q L N E S F S	135
GTG TTC AAC ACA GAA GCA GAG CAG AAT TTC ATT GTC CAG CAG CTG AAT GAG TCA TTT TCT	558

**Fig. 4A**

Y F L G L S D P Q G N N N W Q W I D K T 155  
 TAT TTT CTG GGG CTT TCA GAC CCA CAA GGT AAT AAT AAT TGG CAA TGG ATT GAT AAG ACA 618  
  
 P Y E K N V R F W H L G E P N H S A E Q 175  
 CCT TAT GAG AAA AAT GTC AGA TTT TGG CAC CTA GGT GAG CCC AAT CAT TCT GCA GAG CAA 678  
  
 C A S I V F W K P T G W G W N D V I C E 195  
 TGT GCT TCA ATA GTC TTC TGG AAA CCT ACA GGA TGG GGC TGG AAT GAT GTT ATC TGT GAA 738  
  
 T R R N S I C E M N K I Y L \* 210  
 ACT AGA AGG AAT TCA ATA TGT GAG ATG AAT AAG ATT TAC CTA TGA 783  
  
 GTAGAAGCTTAATTGGAAAAGAGAAGAATFACTGACGTAATTTTTTCCCTGACGCTTTAAAAATTGAACCCCTATCAT 862  
 GAAATGATAAATTTCTTCCCTGAATTTACACATAATCCTTATGTTATAGAGGTTACAGAAAATGAAAAGATACCTGTTTCC 941  
 CTTTAAATCAATCTTCTCGTTTCTTCCATTAATGATAGAAATGCACCCCTTCTCTCTTTGTTCCATTCCTTTCACTT 1020  
 GTTATTCAATTTTTTCTTCCACCTTCATTACACAAAATATTATTGTTTTCAGAGACTGTACTATTTTGTGTTTAG 1099  
 AAGATTTATAAGGCAGTATCTTTTGAAAATTATGACTTTCCTTCCTCAATATACCATAAAGAAATCTTTTGGTCAAGA 1178  
 TGGTAGTTGGAACCTACAATCATCTGAAGGCCCTGACAAGAGTTGAAAGACATGTTTCTAGATGGCTCACTCACATGGCT 1257  
 GGCAACTTGGTGTGGCTATTAAATGTAACTGGAAATAAAATTTTATTTCTGCAGTTAGGGATTTGGCATTTTATATATGT 1336  
 TGATTCAATCAAGTTTGGCAAGCAGGTGTTTCGATACTGCTATATCCTGTATTCTTGGTTTATTGTTTATTCTGAG 1415  
 AAATATGTGTTAAGATCTCTCGCTGATTGGGAATTTGTCTATTTCTCATTTTAAATTTTGTCAAATCTTTCTTTGCTTGC 1494  
 AAGCATTTCTTGTACCCAAATCTAACCTATTCCCTGAAAATATGATGGTTAGCAAAGTTTGAGATACTAGAGCCTGTA 1573  
 ATCCATCATTTTAAATGGCAATGATAATGACAGTTTATTTTATGTTATATAAAAACCTCAACAAAATTTTCCAAACAAT 1652  
 TACCAAAATGGTCATTAATCTGTATCCACAAAGGATTTCTGCATTACATACTTTTAAAACAAATTACCTAATTATTAGT 1731

Fig. 4B

1810 1889 1968 2047 2126 2205 2284 2363 2442 2521 2600 2679 2758 2837 2916 2995 3074 3114

GCATATTAACTTATTGGTGGCATGACTATATGCAACAGTTGCATGATATATGATACAAATTATGTTATTCTTTTCCA 1810  
 TTGCACTGAAAAATACCATATAATAAAGAGAATCCCATCATCCAAATTGAGCCTATATTGATTGATACCTCAGAAAGAAATC 1889  
 TGGCAGTAGGAGCCTATAAAGGATAAGCAAATTGGGAAAGGATTGGGAAGTTGGTAGTACTGAACATCTTCTCACCTGG 1968  
 ACTCATGAGCAACTTGAATAGTTGTAACTGTGATGCATATGTAGATTCTAACACATTTTCCCTTGAATAGAAATTT 2047  
 GGCACAACAATTTTAAATTAATTAGCAAAATATTGGATATTAAAGCTTCTTATAGAAAGAGATACCTGTATATTTA 2126  
 AGCCATGATGAGGTATATACAAATGTTAATTAATTGTTACATGCGAAATTAATTTTATCATTTGTGGAGTCACCT 2205  
 TTCTTTTAAATTTAGTAAATGCCCTTTGGCTTTAAATTTTCTCCTGTATATAAATAAGATACAGTAACTTTTCATTATGTTAG 2284  
 TGCTGTAAAAATTTTTCATCTTCCATCTTCTATTTTGGACCATTTTATTCACATGTGCTCTTAATAAGTAGCATATAGTT 2363  
 AAAATTTAAAAAATCCAATATGGCAATCACCTTTTAGGTTAAAAATTTAATCCATTTACATTTGTGACAAATTCGACATA 2442  
 TATAATGGTTCTAAATCTATCATCTTACTAGGTGGTTTCCATTTCTCTGCTCCAAAATATTTTTTTACAGCTTATAAC 2521  
 ACAACTTTTATAGAAAAAGTTATACATAAACACAGCATCAACTATTTTCAAGAAACCAATAAGCAACAAAAACAGACTA 2600  
 ACAAAAATGTAAACAAGAACTAATGACCTTTCTAAAAATCAAAACATTCAAATTATCTACAATGTCTATTTACAAAAACAGGG 2679  
 AAAACTCCATGGTTTACAGGCATGTCATATTGAAAAATAAAGCTGCAATAGCTTTTATACAAATTATCGCTCTCAAGAAA 2758  
 ATGAAATCATTAAGACAGTAAATTAGGAGTTACAAAAATTTAAAAACATTTACGTAATTTTAAATTAATTGTCTTCAATAATT 2837  
 TTAAATTAATTGAAAGTCTGAGTTTCAAAAAGTGAATTTTTCCTCCACAAGGTGCCAACACATTAAGCTAGAGCTTTCAGTGT 2916  
 AACTTTGCCCTAAAAGTTAAGACATATTCTGAGAAATCATAAATAGTCACATGATTTCTGATGCTATCTGCTCTGTTAAATA 2995  
 ACAAGATTTACACACATGAATACCTATATGTAACAAATCTCCATGTTCTACACATATACCCAGAACTTAAAGTATAATAA 3074  
 TAATAAAACATAGCAAAGCCTTTTAAAAAATAAAAAAATAAAAAA 3114

**Fig. 4C**

FIG. 4D

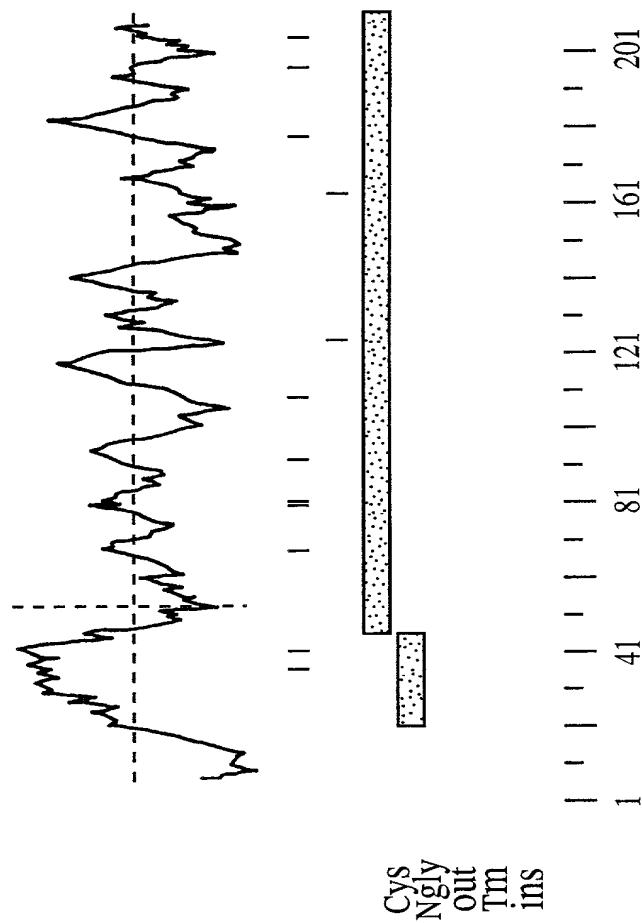


FIG. 4D

I	N	T	E	A	E	Q	N	F	I	T	Q	Q	L	N	E	S	L	S	Y	136
ATC	AAT	ACT	GAA	GCG	GAG	CAG	AAT	TTC	ATC	ACC	CAG	CAG	CTG	AAT	GAG	TCA	CTT	TCT	TAC	581

**Fig. 4E**

Parameter	Value	Unit
Temperature	25.0	°C
Pressure	1.013	bar
Humidity	65.0	%
Wind speed	1.5	m/s
Wind direction	135	°
Cloud cover	3.0	%
Relative humidity	65.0	%
Atmospheric pressure	1013.25	hPa
Sea level pressure	1013.25	hPa
Barometric pressure	1013.25	hPa
Altitude	0.0	m
Latitude	41.88	°N
Longitude	87.63	°W
Time zone	-5.0	h
Daylight saving time	0.0	h
Standard time	-5.0	h
Local time	-5.0	h
UTC time	0.0	h
Time of day	12.0	h
Month	12	
Year	2019	
Day of year	354	
Week of year	52	
Day of month	31	
Month of year	12	
Quarter of year	4	
Season	Winter	
Climate zone	Temperate	
Biome	Deciduous forest	
Vegetation type	Deciduous forest	
Soil type	Loam	
Soil texture	Loam	
Soil color	Brown	
Soil pH	6.5	
Soil moisture	15.0	%
Soil temperature	10.0	°C
Soil depth	0.0	m
Soil horizon	A	
Soil profile	A	
Soil classification	Loam	
Soil use	Agriculture	
Soil management	Conservation	
Soil conservation	Conservation	
Soil erosion	Low	
Soil erosion rate	0.0	t/ha/yr
Soil erosion control	Conservation	
Soil erosion management	Conservation	
Soil erosion prevention	Conservation	
Soil erosion reduction	Conservation	
Soil erosion mitigation	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
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Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
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Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
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Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
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Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
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Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods	Conservation	
Soil erosion control techniques	Conservation	
Soil erosion control strategies	Conservation	
Soil erosion control practices	Conservation	
Soil erosion control measures	Conservation	
Soil erosion control methods</		

[illegible]

**Fig. 4F**

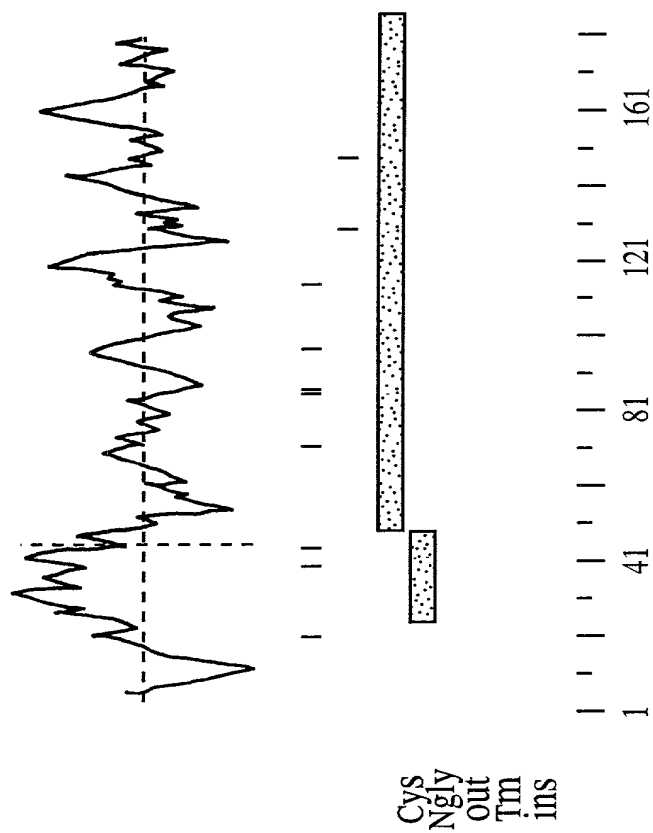


FIG. 46

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	10	20	30	40	50	60	70
human	MMQEQPQST	ETKRGWLS	RLWSVAGI	SALLSACF	IVSCVV	TYHFTY	GETGKRLSELHSHSSLT
	10	20	30	40	50	60	70
murine	MVQERQSQ	GKVC-W	-TLRLWSAA	VISMILL	STCFIASC	VVTYQF	IMDQPSRRLYELHSHSSLT
	10	20	30	40	50	60	70
human	TKVPA--	WGCCPAS	WKSEFG	SSCYFIS	SEEKVS	KSEQNC	VEMGAHLVVFNT
	80	90	100	110	120	130	140
murine	TMVSEKM	WGCCPN	HWKSEF	SSCYLIS	TKENFW	STSEQNC	VQMGHAHLVVINT
	70	80	90	100	110	120	130
human	GLSDPQ	GNNNNQ	WIDKTP	YEKNVR	FWHLGEP	NHSAEQ	CASIVFWKPT
	140	150	160	170	180	190	200
murine	GLSDPK	VMAN--	-----	NGSMILL	SV---K	MSGSG--	-----TPMNP
	140	150	160	170	180	190	200
human L							
murine Q							

Fig. 4H



human	ATGATGCAAGAGCAGCAACCTCAAAGTACAGAGAAAAGAGGCTGGTTGTCCCTGAGACTCTGGTCTGTGG	10	20	30	40	50	60	70
murine	ATGGTGCAGGAAAAGACAATCCCA-----AGGGAAGGGAGTCTGCTGGACCCCTGAGACTCTGGTCAGCTG	10	20	30	40	50	60	
human	CTGGGATTTCATTGCACTCCTCAGTGCCTTGCTTCAATTGTGAGCTGTGTAGTAACATTACCAATTTACATA	80	90	100	110	120	130	140
murine	CTGTGATTTCCATGTTACTCTTGAGTACCTGTTTCATTGCGAGCTGTGTGGTGAACATTACCAATTTATTAT	70	80	90	100	110	120	130
human	TGGTGAAACTGGCAAAAGGCTGTCTGAACTACACTCATATCATTCAAAGTCTCACCTGCTTCAGTGAAGGG	150	160	170	180	190	200	210
murine	GGACCAGCCCAGTAGAAGACTATATGAACCTTCACACATACCATTCCAGTCTCACCTGCTTCAGTGAAGGG	140	150	160	170	180	190	200
human	ACAAAGGTGCCAGCC-----TGGGGATGTTGCCCAGCTTCTTGGAAAGTCATTTGGTTCAGTTGCTACT	220	230	240	250	260	270	
murine	ACTATGGTGTCAAGAAAAAATGTGGGGATGCTGCCCAAATCACTGGAAGTCATTTGGCTCCAGCTGCTACC	210	220	230	240	250	260	270

Fig. 4I

```

280      290      300      310      320      330      340
human  TCATTTCCAGTGAAGAGAGGTTTGGTCTAAGAGTGAGCAGAACTGTGTGAGATGGGAGCACATTTGGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine  TCATTTCTACCAAGGAGAACTTCTGGAGCACCACTGAGCAGAACTGTGTTCAGATGGGGGCTCATCTGGT
280      290      300      310      320      330      340

350      360      370      380      390      400      410
human  TGTGTTCAACACAGAAAGCAGAGCAGAAATTTTCATTGTCCAGCAGCTGAATGAGTCATTTTCTTATTTCG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine  GGTGATCAATACTGAAGCGGAGCAGAAATTTTCATCACCCAGCAGCTGAATGAGTCACTTTCTTACTTCCTG
350      360      370      380      390      400      410

420      430      440      450      460      470      480
human  GGGCTTTCAGACCCACAAGGTAATAATAATTGGCAATGGATTGATAAGACACCTTATGAGAAAAATGTCA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine  GGTCTTTCGGATCC-CAAGGTAATGGCAAAATGGCAATGGATCGATGATACTCCTTTCAGTCAAAAATGTCA
420      430      440      450      460      470      480

490      500      510      520      530      540      550
human  GATTTGGCACCTAGGTGAGCCCAATCATTTCTGCAGAGCAATGTGCTTCAATAGTCTTCTGGAAACCTAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
murine  GGTTCGGCACCCCATGAACCCCAATCTTCCAGAAGAGCGGTGTGTTTCAA-----
490      500      510      520      530
```

Fig. 4J

600 590 600 610 620

560 570 580 590 600 610 620  
human AGGATGGGGCTGGAATGATGTTATCTGTGAACTAGAAAGGAATTCAATATGTGAGATGAATAAGATTAC

murine -----

human CTA

murine ---

**Fig. 4K**

mT405	MVQERQSQGKGVCTLRWSAAVISMLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEGT	10	20	30	40	50	60	70
Dectin	MVQERQSQGKGVCTLRWSAAVISMLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEGT	10	20	30	40	50	60	70
mT405	VSEKMWGCCPNHWKSFSGSSCYLISTKENFWSTSEQNCVQMG AHLVVINTEAEQNFTQQLNESLSYFLGL	80	90	100	110	120	130	140
Dectin	VSEKMWGCCPNHWKSFSGSSCYLISTKENFWSTSEQNCVQMG AHLVVINTEAEQNFTQQLNESLSYFLGL	80	90	100	110	120	130	140
mT405	SDPKVMAN---GNGSMILLSVKMSGSGTPMNP-----IF-----QKSGVFQ	150	160	170	180	190	200	
Dectin	SDPQNGKQWQIDDTFFSQNVRFWHPHEPNLPEERCVSIVYWNPSKWGWNDVFCDSKHNSICEMKKIYL	150	160	170	180	190	200	

Fig. 4L

10	20	30	40	50	60	70
hT405	MMQEQQPQST	TEKRGWLSRL	MSVAGISIAL	SACFIVSCV	VTYHFTYGE	TGKRLSELH
	SYHSSLT	CFSEG				
Dectin	MVQERQSQG	KGVC-W-TL	RLWSAAVIS	MLLSTCFI	ASCVVTYQ	FIMDQPSR
	RLHYELH	TYHSSLT	CFSEG			
10	20	30	40	50	60	70
80	90	100	110	120	130	140
hT405	TKVPA--WG	CCPASWKS	FGSSCYFI	SSEKVS	SKSEQNC	VEMGAHLV
	VFNTEAE	QNFIVQ	QLNES	FSYFL		
Dectin	TMVSEKMW	GCCPNHWK	SFGSSCYL	ISTKEN	FWSTSE	QNCVQMA
	HLVVIN	TEAEQNF	ITQQLN	ESLSYFL		
80	90	100	110	120	130	140
150	160	170	180	190	200	
hT405	GLSDPQGN	NNWQIDK	TPYEKN	VRFWHL	GEPNHS	AEQCA
	SIVFWK	PTGWG	WN	NDVIC	ETRRNS	ICEMNK
Dectin	GLSDPQGN	KWQWIDD	TPFSQNV	RFWHP	HEPNL	PEERC
	VSIVYWN	PSKWG	WN	DFCD	SKHNS	ICEMKK
150	160	170	180	190	200	

Fig. 4M

CGACCCCGCG	TCCGCTGACT	TCTGGGTTTG	CAGCATTGGC	CCGCTCTGTG	GCATTAACT	60
CAAGTGTGTG	TGGAAGTTGA	TTCTGAACTC	TGGCCTCTTT	GACAGAAGCC	AGGTCCTGGA	120
GTCGTATTTT	GGAGACAGAT	GCAAGAAACC	CCTGACCTTC	TGAACATACA	CCTCAACA	178
ATG GTG CAG GAA AGA CAA TCC CAA GGG AAG GGA	GTC TGC TGG ACC CTG	226				
Met Val Gln Glu Arg Gln Ser Gln Gly Lys Gly Val Cys Trp Thr Leu	15					
1	5	10				
AGA CTC TGG TCA GCT GCT GTG ATT TCC ATG ATG TTA CTC TTG AGT ACC TGT	274					
Arg Leu Trp Ser Ala Ala Val Ile Ser Met Leu Leu Ser Thr Cys	30					
20	25					
TTC ATT GCG AGC TGT GTG GTG ACT TAC CAA TTT ATT ATG GAC CAG CCC	322					
Phe Ile Ala Ser Cys Val Thr Tyr Gln Phe Ile Met Asp Gln Pro	45					
35	40					
AGT AGA AGA CTA TAT GAA CTT CAC ACA TAC CAT TCC AGT CTC ACC TGC	370					
Ser Arg Arg Leu Tyr Glu Leu His Thr Tyr His Ser Ser Leu Thr Cys	60					
50	55					
TTC AGT GAA GGG ACT ATG GTG TCA GAA AAA ATG TGG GGA TGC TGC CCA	418					
Phe Ser Glu Gly Thr Met Val Ser Glu Lys Met Trp Gly Cys Cys Pro	80					
65	70	75				

Fig. 4N

Table 4.1

AAT CAC TGG AAG TCA TTT GGC TCC AGC TGC TAC CTC ATT TCT ACC AAG	466
Asn His Trp Lys Ser Phe Gly Ser Ser Cys Tyr Leu Ile Ser Thr Lys	95
	90
	85
	100
GAG AAC TTC TGG AGC ACC AGT GAG CAG AAC TGT GTT CAG ATG GGG GCT	514
Glu Asn Phe Trp Ser Thr Ser Glu Gln Asn Cys Val Gln Met Gly Ala	110
	105
	120
CAT CTG GTG GTG ATC AAT ACT GAA GCG GAG CAG AAT TTC ATC ACC CAG	562
His Leu Val Ile Asn Thr Glu Ala Glu Gln Asn Phe Ile Thr Gln	125
	115
	130
CAG CTG AAT GAG TCA CTT TCT TAC TTC CTG GGT CTT TCG GAT CCA CAA	610
Gln Leu Asn Glu Ser Leu Ser Tyr Phe Leu Gly Leu Ser Asp Pro Gln	140
	135
	150
GGT AAT GGC AAA TGG CAA TGG ATC GAT GAT ACT CCT TTC AGT CAA AAT	658
Gly Asn Gly Lys Trp Gln Trp Ile Asp Asp Thr Pro Phe Ser Gln Asn	160
	145
	165
GTC AGG TTC TGG CAC CCC CAT GAA CCC AAT CTT CCA GAA GAG CGG TGT	706
Val Arg Phe Trp His Pro His Glu Glu Pro Glu Glu Arg Cys	170
	175

Fig. 40

Protein Data Bank

GTT	TCA	ATA	GTT	TAC	TGG	AAT	CCT	TCG	AAA	TGG	GGC	TGG	AAT	GAT	GTT	754
Val	Ser	Ile	Val	Tyr	Trp	Trp	Pro	Ser	Lys	Trp	Gly	Trp	Asn	Asp	Val	
			180				185									
TTC	TGT	GAT	AGT	AAA	CAC	AAT	TCA	ATA	TGT	GAA	ATG	AAG	AAG	ATT	TAC	802
Phe	Cys	Asp	Ser	Lys	His	Asn	Ser	Ile	Cys	Glu	Met	Lys	Lys	Ile	Tyr	
			195				200									
CTA	TGA	GTGCC	TGTTA	TTCAT	TAAATA	TCTTT	TAAAGT	TCAGAC	CCTAC	CAAGA	AGCCA					858
Leu	*															
TAACT	TCTTG	GCCTG	TACAT	CTGAC	AGAGG	CCGTT	CTTTT	CCTAG	CCACT	ATTCT	TTTACT					918
CAAAC	AGAAT	GAGCC	CTTTC	TCCTT	CTGAT	GGTTA	GAGTT	TTGTCA	AACTT	GACACA	AAACT					978
AGAGT	CACCT	GGGAG	TAGG	ATCTT	CAGCT	AAGGA	ATTGC	CTCTG	TCAGC	TTGACC	CAGTC					1038
AGCAT	GTCTG	GGGCA	TTTT	CTTGAT	TAAAT	GATTG	TGTA	AGAGG	GTCCA	GGTG	GTAAGC					1098
AAAGG	TGTTA	AACCC	ATGAA	GAGCA	AGCCA	GGGAG	CATCA	TCCAT	CCATC	TCTG	CCCCTCA					1158
GGTTT	CTGCC	CCAGG	GTCTT	GCCCT	GGTTT	CTTCT	TATGA	ACTG	CTGTA	CTTG	AAAAGTA					1218
TAAGAT	GAAAT	AAACA	ATTTC	ATCCA	AAAAA	AAAA										1252

Fig. 4P



GTCGACCCACGCGTCCGGAACCATTCACAATCACCCCTCCTGAGGAACCTTAGCACTGCATAAAGT	68
GTTCTGAGTTTGTAATCAGATATTGTCACACTGGTTCCTTCAAAACAGACATGACAAGGAGCTGGCTTGG	138
GCTAGGCTGCTCCTTGCCCTATGATTGGGAAGGTTAAACCCCTACAGGGCTTATGTATGTGAAACTGTT	208
GGAACACTGATTAAATGGGATGGACTTCACCTTAACACTCTTGGATTTCCAATATTATGTTTGAGTAAAG	278
AACTGCTATCCACAAACACCATTAATCCTTTAGGAGGCAGAAAAGGCCAGA ATG CAA AGC CAT CTT	345
F I T L G S V F L L L L W A F I W G G	23
TTC ATT ACA CTA GGG TCT GTC TTT TTA CTT CTC TGG GCC TTT ATC TGG GGA GGG	399
H V S P T W N S E P G Q D S N L W A	41
CAT GTT TCC CCC ACT TGG AAC AGT GAG CCT GGC CAG GAC AGT AAC CTG TGG GCT	453
C D D I I S N R E W E R M L A S Q V	59
TGT GAT GAC ATT ATT TCT AAT AGG GAA TGG GAA AGG ATG TTA GCT TCT CAG GTT	507
L K C P G G E E K G R H E K E T M K	77
TTA AAG TGT CCT GGA GGA GAA GAG AAA GGA CAT GAG AAG GAG ACA ATG AAG	561
K M G E G E I V	85
AAG ATG GGT GAG GGG GAG ATA GTG TAAGACCCCTGAGAATGGCATAGGGTAAACTGGGACAG	623
AGATACTGTGGAGAACGATAGCTGCAGAGGGACAGAGGGAGGAGGAAGGAGAGAGAGAGGAGATAAAA	693
ACAGTTTGGAGAACTCTCACAATACATTCAATAAGAAGACAAAGAACCCCAATAAAAAATGGCAACAGATA	763
CCACAGAAAGATGATATATTGAGTGGCCCAATAAATACATAAAAAATATGCTCAACATCTATAATTACCAGGG	833
AAATGCAAATTAAAAGCACTGTGAGATACCACTACACACTGATGAGAAATGGCTAAAATCAAAAAGACCA	903
ACCAGCACTTTGGGAGGCCGAGGTGGCGGATCATGAGGTCAGGAGTTTGAGACTAGCCTGACCAACATG	973

Fig. 5A

GTGAAACCCCTGTCTCTACTAAACATACAAAAATTAGCTGGGGGTGGTGGCATGCGCCTGTAATTCCAGCT 1043  
ACTCAGGAGGCTGAGGCAGGAGAAATCGCTTGAAACCCAGAGGCAGAGATTACAGTGAGCCGAGATCATGC 1113  
CCTTGCACTCTAGCCCTGGGTGACAGAGCGAGACTCTGTCTTAAAAAATAAAAAAATAAAAAAATAAAAAA 1183  
AAAAAAAGGGCGGCCGC 1202

**Fig. 5B**

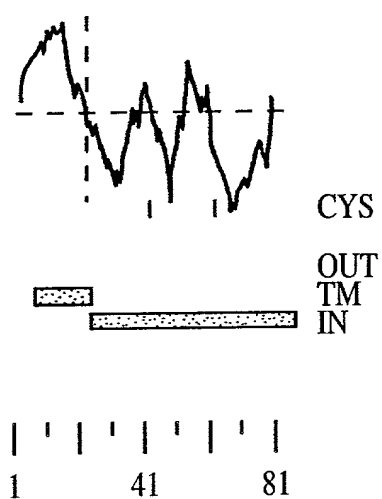


FIG. 5C